

Testing Protein-Structure Hypotheses using Rare Variants Identified from Genomic Sequencing Studies

ABSTRACT

Multiple large-scale whole-genome sequencing projects are underway for a variety of human phenotypes. These studies are identifying hundreds of thousands of new genetic variants, but our ability to statistically characterize their influence on these phenotypes is limited by their low frequency. In this talk, we will discuss ways to integrate genetic variation with existing protein structure data, new approaches for genetic data analysis within this protein structural context, and provide an overview of the computational infrastructure needed to manage this new scale of data in the Alzheimer's Disease Sequencing Project.

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